

158220

From: Mertz, Prema
Sent: Tuesday, July 05, 2005 2:37 PM
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Please search SEQ ID NO:1-2 with protein databases.

Thanks.

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Searcher: _____
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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
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Other(Specify): _____

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GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: July 9, 2005, 12:41:15 ; Search time 111.181 Seconds
(wtihout alignments)
801.415 Million cell updates/sec

Title: US-10-750-797-1
Perfect score: 896
Sequence: I TPIGPASSLPLQSPFLKLCLEQ. SHIQQSFFLEVSYRVLRLHQAQ 174

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:
OK

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	896	100.0	200	Q8N4W3
2	884.5	98.7	207	Q8P3_HUMAN
3	744	83.0	194	Q8P3_FELCA
4	744	83.0	195	Q9GJU0
5	738	82.4	174	Q8P3_SHEEP
6	734	81.9	175	Q8P3_CANFA
7	727	81.1	195	Q8P3_BOVIN
8	702	78.3	195	Q8P3_PIG
9	641	71.5	208	Q8P3_MOUSE
10	634	70.8	214	Q977I2
11	511	57.0	127	Q8MKED
12	304	33.9	201	Q8MKCHICK
13	111	12.4	241	Q90YI0
14	110.5	12.3	212	Q8mW75
15	108	12.1	208	Q9xt80
16	106.5	11.9	212	1T6_PIG
17	101	11.3	205	1T6_ORC
18	100	11.2	208	1T6_HORSE
19	95	10.7	189	Q6NZB2
20	96	10.7	189	Q9H2A5
21	95	10.6	208	1T6_FELCA
22	94.5	10.5	455	Q8D706
23	94	10.5	345	Q9KT16
24	93	10.4	189	Q9npF7
25	91	10.2	189	Q6NZB0
26	89.5	10.0	214	Q8mKES
27	89.5	10.0	2175	1RNCU_DROME
28	88.5	9.9	666	Q9A5Z3
29	88.5	9.9	786	Q9I019
30	88.5	9.9	1931	Q8RJY3
31	9.6	208	IIIG_BOVIN	P26892

RESULT 1				
ID	Q8N4W3	PRELIMINARY;	PRT;	200 AA.
AC	Q8N4W3;			
DT	01-OCT-2002 (T-EMBL; 22, last sequence update)			
DT	01-MAR-2004 (TREMBL; 26, last annotation update)			
DE	Colony stimulating factor 3, isoform c.			
GN	Name-CSF3;			
OS	Homo sapiens (Human).			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID=9606;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SKIN;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	straubenberg R.L., Feingold E.A., Grouse L.H., Derre J.G., Schueler G.D., Klauser R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Blueton K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marsubina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C., Strubenberg R.L., Loquellano N.M., Peters G.J., Abramson R.D., Mullahay S.J., Raha S., Loquellano N.M., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McElwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Keeteman M., Mardon A., Rodrigues S., Sanchez A., RA			
RA	Blakeslee R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinbaum J.J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallius D.E., Schnerech A., Schein J.E., Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RA	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
RA	EBML; BC033245; AAH33245.1; -.			
RA	HSSP; P05919; 1GN.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005125; F:cytokine activity; IEA.			
DR	GO; GO:0005139; F:interleukin-6 receptor binding; IEA.			
DR	GO; GO:0006959; P:immune response; IEA.			
DR	InterPro; IPR00919; 4_helic_cytokine.			
DR	InterPro; IPR03629; GCSF_MGF.			
DR	InterPro; IPR003573; 1T6_MGF_GCSF.			
DR	InterPro; IPR003574; Interleukin_6.			
DR	PFam; PF0489; IL6; 1.			
PRINTS; PR00433; IL6GCSFNGF.				

Q34008	beta vulgaris
Q8CF87	mus musculus
Q7tq21	mus musculus
Q8cf88	mus musculus
Q81lt9	mus musculus
Q865w7	camelus bacillus
Q81lqb8	oryza sativa
Q9n2h9	sus scrofa
Q6v919	babirusa bubalis
Q28819	phoca vitulina
Q865x6	lama glama
Q7mdw7	vibrio vulnificus
Q9tth4	aotus nigri
Q28319	capra hircus

DR PRINTS; PR00434; INTERLEUKIN-6.
 DR PRODOM; PDD00388; GCSF MGF; 1.
 DR PRODOM; PDD04356; Interleukin-6; 1.
 DR SMART; SNO0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN-6; 1.
 SQ SEQUENCE 200 AA; 2153 MW; 864RRA55B329A96C CRC64;
 RQ Query Match 100.0%; Score 896; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 5.2e-74; RA
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPIGASSLQSPLRIKLCQVKLGQDGAMQEKLGATVYKUCHPRLVILGHSGIPWAR 60
 DB 27 TPIGASSLQSPLRIKLCQVKLGQDGAMQEKLGATVYKUCHPRLVILGHSGIPWAR 60
 RQ 61 LSSCBSQLQLAGCTISOLHSGFLYVGGLQALBGTSPELGPTDQLQDVAFDATTIWO 120
 DB 87 LSSCFSQALQLAGCISQHSGFLQVQLQALBGSPELGPDTQDVAFDATTIWO 146
 QY 121 MEELGMAPALQOPTOGAMPFAFORRAGGTIVASHLQSTEVSTRVLHLAQ 174
 DB 147 MEELGMAPALQOPTOGAMPFAFORRAGGTIVASHLQSTEVSTRVLHLAQ 200

RESULT 2

CSF3 HUMAN STANDARD; PRT; 207 AA.

ID CSF3 HUMAN STANDARD; PRT; 207 AA.

AC P09919;

DT 01-MAR-1989 (Rel. 10, Last sequence update)
 25-OCT-2004 (Rel. 45, last annotation update)

DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoietin)
 DE (Filgrastim) (Lenograstim).
 GN Name=CSF3;

OS Homo sapiens (Human); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE:86110679; PubMed=3484805;
 RA Nagata S., Tauchiya M., Asano S., Kaziro Y., Yamamoto O.,
 RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.,
 RT "Molecular cloning and expression of cDNA for human granulocyte
 colony-stimulating factor.";
 RL Nature 319:415-418(1986).

[2]

RN SEQUENCE FROM N.A.
 RX MEDLINE:8622037; PubMed=2423327;
 RA Nagata S., Tauchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamazaki T.;
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 colony-stimulating factor.";
 RL EMBO J. 5:575-581(1986).

[3]

RP SEQUENCE FROM N.A.
 RX MEDLINE:87196936; PubMed=3494801;
 RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 RT lines.";
 RL J. Leukoc. Biol. 41:302-306(1987).

[4]

RP SEQUENCE FROM N.A. AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs: NHBLI Hap6682 program for genomic applications, UN-
 FERC, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [5]

RP SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE:86151684; PubMed=2423009;

RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zeebo K.M.,

RA Murdock D.C., Chazin V.R., Brubzowski J., Lu H., Chen K.K.,
 RA Bartendt J., Blatter E., Moore M.A.S., Merrelmann R., Weltz K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 normal and Leukemic myeloid cells.";
 RL Science 232:61-66(1986).

[6]

RN CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE:93293942; PubMed=7185769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 of recombinant human granulocyte colony-stimulating factor glycoforms
 produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62(1993).

[7]

RN STRUCTURE BY NMR.
 RX MEDLINE:93102001; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-M;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 derived from NMR Spectroscopy.";
 RL FEBS Lett. 314:435-439(1992).

[8]

RN [8]

RP STRUCTURE BY NMR.
 RX MEDLINE:94304859; PubMed=718249;
 RA Zink T., Ross A., Luers K., Cieclar C., Rudolph R., Holak T.A.;
 RT "Structure and dynamics of the human granulocyte colony-stimulating
 factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 bundle protein.";
 RL Biochemistry 33:8453-8463(1994).

[9]

RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE:93281718; PubMed=7085117;
 RA Hill C.P., Oslund T.D., Eisenberg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 relationship to other growth factors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).

CC -- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSF induce granulocytes.
 CC -- SUBUNIT: Monomer.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
 CC Name=Short; IsoId=P09919-1; Sequence-Displayed;
 CC Name=Long;
 CC IsoId=P09919-2; Sequence=VSP 002673;
 CC -- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
 CC modified with up to two sialic acid residues (done in
 CC recombinantly expressed G-CSF from CHO cells).
 CC -- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -- CAUTION: Ref 4 misquotes the gene name as "CSF1".
 CC -- DATABASE: NAME=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW="http://www.neupogen.com".

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 CC -----
 DR X03438; CAM2716; 1; --
 DR M1308; AAC0356; 1; --
 DR X03655; CAA27291; 1; --
 EMBL; X03655; CAA27290; 1; --

DR EMBL; AF388025; AAH62469.1; -.
 DR EMBL; ML7706; AAH3882.1; -.
 DR PIR; A24573; A24573.
 DR PIR; A25093; QHUGL.
 DR PDB; 1CD9; X-ray; A/C/E/G=3/-207.
 DR PDB; 1GNC; NNR; @=30-207.
 DR PDB; 1IGR; X-ray; A/C/E/G=3/-207.
 DR PUB; IRHG; X-ray; A/B/C=31-207.
 DR Genew; HGNC:2438; CSF3.
 MIM; 138970; C:extracellular space; TAS.
 GO; GO:0005615; P:granulocyte colony-stimulating factor recep. . ; TAS.
 GO; GO:0005130; P:development; TAS.
 GO; GO:0007275; P:development; TAS.
 GO; GO:0008484; P:positive regulation of cell proliferation; TAS.
 InterPro; IPR09079; 4 helix cytokine.
 InterPro; IPR03229; GCSF_MGF.
 InterPro; IPR03573; IL6_-MGF_GCSF.
 Pfam; PF00489; IL6; 1.
 PRINTS; PR00433; IL6GCSFMGF.
 PRODOM; PD008388; GCSF_MGF; 1.
 SMART; SM00126; IL6; 1.
 PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW 3D-structure; Alternative splicing; Cytokine; Glycoprotein;
 KW Growth factor; pharmaceutical; Polymorphism; signal.
 SIGNAL 1 30
 FT CHAIN 3 1 207
 FT DISULFID 6 9 75
 FT CARBOHYD 166 166 166
 FT VARSPLIC 66 68 68
 FT VARIANT 157 157 157
 FT FTID=VAR_013074.
 FT HELIX 41 65 69
 FT HELIX 69 71 77
 FT HELIX 77 86 87
 FT TURN 105 124 88
 FT TURN 125 127 130
 FT TURN 130 132 133
 FT TURN 156 158 157
 FT TURN 176 203 204
 FT SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;
 Query Match 98.3%; Score 884.5; DB 1; Length 207;
 Best Local Similarity 98.3%; Pred. No. 6.1e-73;
 Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 FT SIGNAL <1 20
 FT CHAIN 21 194
 FT DISULFID 56 62
 FT CARBOHYD 153 153
 FT SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
 Query Match 83.0%; Score 714; DB 1; Length 194;
 Best Local Similarity 81.0%; Pred. No. 4.2e-60;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 FT SIGNAL <1 20
 FT CHAIN 21 194
 FT DISULFID 56 62
 FT CARBOHYD 153 153
 FT SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
 Query Match 83.0%; Score 714; DB 1; Length 194;
 Best Local Similarity 81.0%; Pred. No. 4.2e-60;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 FT SIGNAL <1 20
 FT CHAIN 21 194
 FT DISULFID 56 62
 FT CARBOHYD 153 153
 FT SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
 DR AC 002707;
 DT 30-MAY-2000 (Rel. 3.9, Created)
 DT 05-JUL-2004 (Rel. 4.4, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).

AC Q9GTU0; DT 01-MAR-2001 (TREMBREL_16, Created)
 DT 01-MAR-2001 (TREMBREL_16, Last sequence update)
 DT 05-JUL-2004 (TREMBREL_27, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor.
 GN Name=G-CSF;
 OS Felis silvestris catus (Cat).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI TAXID=9685;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=21551548; PubMed=11675019; DOI=10.1016/S0378-1119(01)00575-3;
 RA Yamamoto A., Iwata A., Tsuchiya K., Katsunuma A., Oishi K., Saito T..
 RA Yamamoto H., Haegawa A., Ueda S.;
 RT Molecular cloning and expression of the cDNA encoding feline
 granulocyte colony-stimulating factor.;
 RL Gene 274:263-269(2001).
 DR EMBL; AB042553; BAB17757.1; -.
 DR EMBL; AB042552; BAB17789.1; -.
 DR HSSP; P35934; 1BGE.
 DR GO; GO_0005576; C:extracellular.
 DR GO; GO_0005125; F:cytokine activity; IEA.
 DR GO; GO_0005138; F:interleukin receptor binding; IEA.
 DR GO; GO_0006555; F:immune response; IEA.
 DR InterPro; IPR005079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 PFAM; PF00489; IL6_1.
 DR PRINTS; PR00433; IL6GSEFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PRODOM; PDO08388; GCSF_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SIGNAL; 1; 22; Potential.
 FT SIGNALC 195 AA; 21255 MW; 544C6B2909412FCF CRC64;
 SQ SEQUENCE

Query Match 83.0%; Score 744; DB 2; Length 195;
 Best Local Similarity 81.0%; Pred. No. 4_2e-60;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 TPLGPASSLPSOSFLKCLQEVRKIQDGGAQALQKCATYKLCPEELVLLGHSIGIWPW 60
 Db 22 TPIQPTSSLPSOSFLKLCLEQVRKVQADGTAQKQERICAAHKCPPEELVLLGHSIGIWPQ 81

QY 61 LSSCPSQALQASCLSQHSLSLFLYQGLQALAGISPLRGPTDFTLQDVAFATTWQQ 120
 Db 82 LSSCSSQALQTSCLDQHGGFLFLYQGLQALAGISPLAPTLMQLDITDFAINTIWQ 141

QY 121 MEELGMAPALOPTOGMMPAFASAFORRAGGVLYASHLQSFLYIVSYRVLHIAQP 174
 Db 142 MDVGMAPAVPPTGTMFTSAFORRAGGVLYASHLQSFLYIVSYRVLHIAQP 195

RESULT 5

CSF3_SHEEP STANDARD; PRT; 174 AA.

ID _CSF3_SHEEP AC P028746; 30-MAY-2000 (Rel. 39, Created).
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor (G-CSF).
 GN Name=CSF3;
 OS Ovis aries (Sheep).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Carnivora; Fissipedia; Canidae;
 OC Caprinae; Ovis.
 NCBI TAXID=9940;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=95102116; PubMed=7528579;

RESULT 6

CSF3_CANFA STANDARD; PRT; 175 AA.

ID _CSF3_CANFA AC P35834; 01-JUN-1994 (Rel. 29, Created).
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor (G-CSF).
 GN Name=CSF3;
 OS Canis familiaris (Dog).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI TAXID=9615;
 RN [1] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=9407631; PubMed=7550736;
 RX Lovejoy B., Cascio D., Bisemberg D.;

RA O'Brien P.M., Secow H.F., Rothel J.S., Wood P.R.;
 RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
 factor cDNA.";
 RL DNA Seq. 4:339-342(1994).
 CC -I_ FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC GSF induces granulocytes (By similarity).
 CC -I_ SUBUNIT: Monomer.
 CC -I_ SUBCELLULAR LOCATION: Secreted.
 CC -I_ PTM: O-glycosylated (By similarity).
 CC -I_ SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 DR EMBL; ID07939; AAA68006.1; -.
 DR PIR; TI0268; TM0268.
 DR HSSP; P9919; 1RHG.
 DR InterPro; IPR005079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GSEFMGF.
 DR PRODOM; PDO08388; GCSF_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor.
 FT DISULFID 36 42 By similarity.
 FT CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
 FT SEQUENCE 174 AA; 18806 MW; BASAK8FB023AC01E CRC64;

Query Match 82.4%; Score 738; DB 1; Length 174;
 Best Local Similarity 82.2%; Pred. No. 1_3e-59;
 Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 1 TPLGPASSLPSOSFLKCLQEVRKIQDGGAQALQKCATYKLCPEELVLLGHSIGIWPW 60
 Db 1 TPIQPTSSLPSOSFLKLCLEQVRKVQADGTAQKQERICAAHKCPPEELVLLGHSIGIWPQ 60

QY 61 LSSCPSQALQASCLSQHSLSLFLYQGLQALAGISPLRGPTDFTLQDVAFATTWQQ 120
 Db 61 LSSCSSQALQTSCLDQHGGFLFLYQGLQALAGISPLAPTLMQLDITDFAINTIWQ 120

QY 121 MEELGMAPALOPTOGMMPAFASAFORRAGGVLYASHLQSFLYIVSYRVLHIAQP 174
 Db 121 MDVGMAPAVPPTGTMFTSAFORRAGGVLYASHLQSFLYIVSYRVLHIAQP 174

RT "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF)." RP
 RT J. Mol. Biol. 234:640-653 (1993). RC
 RL CC Heidari M., Kahrli M.B. Jr.;
 CC "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte colony stimulating factor." RT
 CC submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. RT
 CC [2] X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS). RN
 CC DR MEDLINE=4076341; PubMed=7504736; RX
 RA Lovejoy B., Cascio D., Eisenberg D.;
 CC "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF)." RT
 CC J. Mol. Biol. 234:640-653 (1993). CC
 CC [1] -I- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
 CC -I- SUBUNIT: Monomer.
 CC -I- PTM: O-glycosylated.
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
 DR PDB: 1BGP; X-ray; @=1-175.
 DR 1BGP; X-ray; A=B=1-175.
 DR InterPro: IPR003629; GCSF_MGF.
 DR InterPro: IPR003531; IL6_MGF_GCSF.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRODOM: PD00388; GCSF_MGF; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW 3D-structure; Cytokine; Glycoprotein; Growth factor.
 FT DISULFID 37 43
 FT DISTYLY 65 75
 FT CARBOHYD 134 134 O-linked (GalNAc. . .) (By similarity).
 FT STRAND 10 10
 FT HELIX 12 39
 FT TURN 93 95
 FT HELIX 45 55
 FT TURN 56 56
 FT HELIX 63 65
 FT TURN 67 69
 FT HELIX 72 92
 FT TURN 93 95
 FT TURN 98 100
 FT HELIX 101 125
 FT TURN 126 126
 FT HELIX 144 171
 FT TURN 172 172
 FT STRAND 173 173
 SQ SEQUENCE i 15 AA; 18858 MW; 28C26B24990C6DB3 CRC64;
 Query Match 81.9%; Score 734; DB 1; Length 175;
 Best Local Similarity 80.9%; Pred. No. 3.1e-59; ID: 11; Mismatches 22; Indels 0; Gaps 0;
 Matches 140; Conservative 11; MisMatches 0;
 QY 2 PLGPASSPLQSPFLKLCLEOKVKGQKLGKPEELVLSIGLIPWAPL 61
 Db 3 PLGPGPGLPQSPFLKLCLEOKVKGQKLGKPEELVLSIGLIPQPL 62
 QY 62 SCSCSQALQLAGCISOLHSGLFLYQGLIQALEGISPSELGPTLDTQDVADEFATTIWOQ 121
 Db 63 SCSCSQALQLQMGLRQHSGLFLYQGLIQALAGISPSELAPTDLTQDVTFAINIWOQ 122
 QY 122 EELGMAPALOPTQGMPAFASAFORRAGSTVASHQSEFLEVSYVTRILAQ 174
 Db 123 EDLGMAPAVPPTQGMPAFASAFORRAGGVVLVASNQSFLELAYRAHLFACKP 175
 RESULT 7
 CSF3_BOVIN
 ID CSF3_BOVIN STANDARD; PRT: 195 AA.
 AC P25833; Q9TVW9;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 DE Name=CSF3; Synonyms=GCSF;
 OS Bos taurus; (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos;
 OC NCBI_TaxId=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein;
 RA Heidari M., Kahrli M.B. Jr.;
 CC "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte colony stimulating factor." RT
 CC submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. RT
 CC [2] X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS). RN
 CC DR MEDLINE=4076341; PubMed=7504736; RX
 RA Lovejoy B., Cascio D., Eisenberg D.;
 CC "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF)." RT
 CC J. Mol. Biol. 234:640-653 (1993). CC
 CC [1] -I- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
 CC -I- SUBUNIT: Monomer.
 CC -I- PTM: O-glycosylated.
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
 CC DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRODOM: PD00388; GCSF_MGF; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 195 Potential. Granulocyte colony-stimulating factor.
 FT DISULFID 57 95
 FT DISTYLY 85 95 O-linked (GalNAc. . .) (By similarity).
 FT CARBOHYD 154 154 -TS -> RG (in Ref. 2).
 FT CONFLICT 93 94
 FT HELIX 32 60
 FT HELIX 65 69
 FT TURN 70 71
 FT HELIX 72 75
 FT TURN 76 76
 FT HELIX 83 85
 FT TURN 87 89
 FT HELIX 92 112
 FT TURN 113 115
 FT TURN 118 120
 FT HELIX 121 145
 FT HELIX 164 191
 FT TURN 192 192
 SQ SEQUENCE i 195 AA; 19431 MW; 8C06119E4ADFBAT3 CRC64;
 Query Match 81.1%; Score 727; DB 1; Length 195;
 Best Local Similarity 81.0%; Pred. No. 1.5e-58; ID: 11; Mismatches 22; Indels 0; Gaps 0;
 Matches 141; Conservative 11; MisMatches 0;
 QY 1 PLGPASSPLQSPFLKLCLEOKVKGQKLGKPEELVLSIGLIPWAPL 60
 Db 22 TPGPARALPQSPFLKLCLEOKVKGQKLGKPEELVLSIGLIPQAP 81
 QY 61 LSSCPSQALQLAGCISOLHSGLFLYQGLIQALEGISPSELGPTLDTQDVADEFATTIWOQ 120

DR InterPro; IPR003629; GCSF MGF.

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; ILGCSFMGP.

DR Prodom; PD008388; GCSF MGF; 1.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR Cytokine; Direct protein sequencing; Growth factor; KW signal.

FT SIGNAL 1 30

FT DISUFLID 72 78 Granulocyte colony-stimulating factor.

FT DISUFLID 100 110 By similarity.

FT CARBOHYD 169 169 O-linked (GalNAc...) (By similarity).

SQ SEQUENCE 208 AA; 22421 MW; 0BP3622135C905DB CRC64;

Query Match Best Local Similarity 75.9%; Pred. No. 1; 2e-50; Length 208; Matches 129; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

QY 3 LGPASSLPOSTLKLCKEQRKIQDGALOBLKATYKUCHPEELVILGHSLGIPWAPS 62

Db 30 LPPSLPLRSPFLKLSLEQVRKIQARNTTELBOLCATYKUCHPEELVLFHSLGIPKASLS 89

QY 63 SCPSQLQLAGCLSQLHSGLFLYQGLIQLALEGISRLGPTDLTLDQDADFTIWQOME 122

Db 90 SCSSQALQQTKCLSQLHSGLFLYQGLIQLALEGISRLGPTDLTLDQDADFTIWQOME 149

QY 123 ELGMAPALQPROGAMPAPASAFOARRAGGVLYASHQSFLEVSYRVRHLAQ 174

Db 150 SLGVAPVTQFOSTMFPTAFORRAGGVLYTYSQSFLETAAHHHLHRP 201

RESULT 11

ID Q8MKED0 PRELIMINARY; PRT; 127 AA.

ID Q8MKED0 AC 08MKED0; DT 01-OCT-2002 (TREMBrel. 22, Created)

Db 99 GCSSQALQQTKCLSQLHSGLFLYQGLIQLALEGISRLGPTDLTLDQDADFTIWQOME 158

DE Granulocyte colony-stimulating factor.

QY 123 ELGMAPALQOPTOGAMPAPASAFOARRAGGVLYASHQSFLEVSYRVRHLA 172

Db 159 NLGVAPTVOPTQSAMPAFTAFOARRAGGVLYTYSQSFLETAAHHHLHLRP 208

RESULT 12

ID P97712 PRELIMINARY; PRT; 214 AA.

AC P97712; DT 01-MAY-1997 (TREMBrel. 03, Created)

DT 01-MAY-1997 (TREMBrel. 03, Last sequence update)

DT 01-MAY-2004 (TREMBrel. 26, Last annotation update)

DE Granulocyte colony stimulating factor.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. NCBI_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Noronha L. E., Takafuji V.A., Sharova I.V., Cristman M. V., Howard R. D., RN [1] DR Submitted (APR-2002) to the EMBL/GenBank/DBJ databases. EMBL; AFS03365; AACM34205.1; -.

DR HSSP; P38833; IBCG.

GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005125; F:Cytokine activity; IEA.

DR GO; GO:0008083; F:Growth factor activity; IEA.

DR GO; GO:0006935; P:immune response; IEA.

DR InterPro; IPR009079; 4_helix_Cytokine.

DR InterPro; IPR003628; GCSF MGF.

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGP.

DR Prodom; PD008388; GCSF MGF; 1.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR Sequence; 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Match Best Local Similarity 70.8%; Score 634; DB 2; Length 214; Best Local Similarity 73.8%; Pred. No. 5.6e-50; Mismatches 35; Indels 0; Gaps 0;

SQ SEQUENCE FROM N.A.

RP MEDLINE=97074656; PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X; RA Han S.W., Kamesh N., Osborne W.R.; RT "Cloning and expression of the cDNA encoding rat granulocyte colony- stimulating factor." RT "Stimulating factor." RT Gene 175:101-104(1996); DR U37101; AAC291515; 1; -. DR PTR; JCS043; JC5043; DR K0SP; P09119; 1RKG. DR GO; GO_0005576; C:extracellular; IEA. DR GO; GO_0005125; F:Cytokine activity; IEA. DR GO; GO_0008083; F:Growth factor activity; IEA. DR GO; GO_0006935; P:immune response; IEA. DR InterPro; IPR009079; 4_helix_cytokine. DR InterPro; IPR00629; GCSF MGF. DR InterPro; IPR003573; IL6_MGF_GCSF. DR Pfam; PF00489; IL6; 1. DR PRINTS; PR00433; IL6GCSFMGP. DR Prodom; PD008388; GCSF MGF; 1. DR SMART; SM00126; IL6; 1. DR PROSITE; PS00254; INTERLEUKIN_6; 1. DR Sequence; 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Match Best Local Similarity 79.5%; Pred. No. 5.9e-39; Length 127; Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 48 VLGHSGTGPWAPISSCPSQLLAGCISQLHSGLFLYQGLIQLLEGISRLGPTDLTQ 107

Db 1 MLGCSFMGPQLSSCSQLQQLTGCSLQLVQGLLQLLAGSPELAFTIDMQ 60

QY 108 LDVADPATIWIQOMEELGMAPALQOPTOGAMPAPASAFOARRAGGVLYASHQSFLEVSYRV 167

Db 61 LDVADPATIWIQOMEELGMAPALQOPTOGAMPAPASAFOARRAGGVLYASHQSFLEVSYRV 120

QY 168 LRHLAQP 174

Db 121 LRHLAQP 127

RESULT 12

ID MGF_CHICK PRELIMINARY; PRT; 201 AA.

AC P3854; DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Myelomonocytic growth factor precursor (MGF).

OS Gallus gallus (Chicken).

		RESULT 13
RN	[1]	SEQUENCE FROM N.A.
RX	[1]	MDLINE-89231616; PubMed=2785450;
RA	[1]	Leutgeb A.; Damm K.; Steineck E.; Kowenz E.; Ness S.; Frank R.,
RA	[1]	Gausepohl H.; Pan Y.-C.E.; Smart J.; Hayman M.; Graf T.;
RT	[1]	"Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals relationship to interleukin 6 and granulocyte colony stimulating factor.";
RT	[2]	EMBO J. 8:175-181(1989).
RN	[2]	SEQUENCE FROM N.A.
RX	[2]	MEDLINE-92195319; PubMed=1549124;
RA	[2]	Sternberg E.; Blattner C.; Graf T.; Leutz A.;
RT	[2]	"Structure of the chicken myelomonocytic growth factor gene and specific activation of its promoter in avian myelomonocytic cells by protein kinases";
RL	[2]	Mol. Cell. Biol. 12:1728-1735(1992).
CC	[2]	-I- FUNCTION: Hematopoietic growth factor that stimulates the proliferation and colony formation of normal and transformed avian cells of the myeloid lineage.
CC	[2]	-I- SUBCELLULAR LOCATION: Secreted.
CC	[2]	-I- SIMILARITY: Belongs to the IL-6 superfamily.
CC	[2]	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	[2]	SEQUENCE FROM N.A.
CC	[2]	EMBL; MB5034; AAA48694_1; -.
DR	[2]	EMBL; X14477; CAN32639_1; -.
DR	[2]	PIR; A42247; A42247.
DR	[2]	HSSP; P09919; 1RIG.
DR	[2]	InterPro; IPR009079; 4 helix cytokine.
DR	[2]	InterPro; IPR003299; GCSF MGF.
DR	[2]	InterPro; IPR03573; IL6 MGR GCSF.
DR	[2]	InterPro; IPR03574; Interleukin_6.
DR	[2]	Pfam; PF00489; IL6_1.
DR	[2]	PRINTS; PR00433; IL6GESEFMGP.
DR	[2]	PRINTS; PR00434; INTERLEUKIN6.
DR	[2]	PRODOM; PD008388; GCSF MGF; 1.
DR	[2]	PRODOM; PD004356; Interleukin_6; 1.
DR	[2]	SMART; SM0126; IL6_1.
DR	[2]	PROSITE; PS00254; INTERLEUKIN_6; 1.
DR	[2]	KW SIGNAL.
DR	[2]	PROSITE; PS00254; INTERLEUKIN_6; 1.
KW	[2]	glycoprotein; Growth factor; Signal.
FT	[2]	SIGNAL 1 23 Myelomonocytic growth factor.
FT	[2]	CHAIN 24 201 By similarity.
FT	[2]	DISULFID 61 67 N-linked (Glycan. . .) (Potential).
FT	[2]	CARBONID 99 123 N-linked (Glycan. . .) (Potential).
FT	[2]	CARBONID 123 137 SEQUENCE 201 AA; 22373 MW; 24040D21B424E6 CRC64;
Query Match	33.9%	Score 304; DB 1; Length 241; Best local Similarity 22.2%; Prod. No. 0.053; Mismatches 74; Indels 52; Gaps 7; Matches 67; Conservative 28; Mismatches 68; Indexes 2; Gaps 1;
Qy	11	QSPFLKCLEQVRKIQGGAGALQEKKVTKLCHREPELVLUGHSLGIPMAPLSSCPSQLQ 70
Qy	36	QFLHKKLKEFTRKRGVDAVQLAVRQCDTQLCLTCEBLLQVDPDHLQAPDCKKRGSQ 95
Dy	71	LACGLSLOQHSGLFLYQGLQIALECTISPEGLGPTLTDQLQDVADEPATITQWQMEBLGMAPAL 130
Dy	96	AECVCFPTORAGLHYAHDGAVLILPNNPLTVEQLDQANLSNTIQOQMEDLGDTVT 155
Qy	131	QPTQ-GAMPAFAASFQRRAGGVIVASHIQLQSFLEVSYVRLHQ 173
RN	[1]	SEQUENCE FROM N.A.
ID	090Y10	PRELIMINARY;
AC	090Y10	PRT; 241 AA.
DT	090Y10; 01-DEC-2001 (TREMBLEL 19, Created)	
DT	01-DEC-2001 (TREMBLEL 19, Last sequence update)	
DT	05-JUL-2004 (TREMBLEL 27, Last annotation update)	
DE	Interleukin-6 precursor.	
Name	IL-6	
GN	Gallus gallus (Chicken)	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
OC		
OC		
OX		
RN	[1]	SEQUENCE FROM N.A.
RA	[1]	SEQUENCE FROM N.A.
RA	[1]	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]	SEQUENCE FROM N.A.
RA	[2]	Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J., Wigley P.;
RA	[2]	"Differential cytokine expression in avian cells in response to invasion by <i>Salmonella typhimurium</i> , <i>Salmonella enteritidis</i> and <i>Salmonella gallinarum</i> ";
RL	[2]	Microbiology 146:3217-3226 (2000).
RN	[3]	SEQUENCE FROM N.A.
RA	[3]	Kaiser P.; Kaspers B., Staeheli P.; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL	[3]	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR	[3]	DR GO; AU309540; CAC40812_1; -.
DR	[3]	DR EMBL; AU250838; CAC15662; -.
DR	[3]	DR HSSP; P05231; IALU.
DR	[3]	DR GO; GO:00055125; F:cytokine activity; IEA.
DR	[3]	DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR	[3]	DR GO; GO:0006595; F:immune response; IEA.
DR	[3]	DR Pfam; PF00489; IL6_1.
DR	[3]	DR PRINTS; PR00433; IL6GESEFMGP.
DR	[3]	DR PRINTS; PR00434; INTERLEUKIN6.
DR	[3]	DR PRODOM; PD008388; GCSF MGF; 1.
DR	[3]	DR SMART; SM0126; IL6_1.
DR	[3]	DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT	[3]	FT SIGNAL 1 47 Potential.
FT	[3]	FT CHAIN 48 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
SQ	[3]	SEQUENCE 241 AA;
Query Match	12.4%	Score 111; DB 2; Length 241; Best local Similarity 22.2%; Prod. No. 0.053; Mismatches 74; Indels 52; Gaps 7; Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;
Qy	3	LGRASSPL-----OSFLKCLEQVRKIQGGAGALQEKKVTKLCHREPELVLUGHSLGIPMAPLSSCPSQLQ 43
Dy	41	LPPRAVLPAPAADSSGEVGLEERAGARRALDCBPLARVLRDRAVOLQDDEMCKKFTVE 100
Qy	44	PEEFLVGHSLGFLYQPLWAPLSSCPSQLQLAG---CISQLHSGLFLYQGLQIALEGIPAE 98
Dy	101	NNSMELVRLNLPL---KVTEBDGCLLAFDPEBKCLLKLISGLFAQTYLEFTQFD 156
Qy	99	LGFLDITQDVADEPATITQWQMEBLGMAPALOPTQGAMPFAASFQRRAGGVIL 152
Dy	157	EKVNQESICSYCSTKHLAAITROMY-----NPDEVWIP-DSAAOKSLLNLKSDKW 206
Qy	153	--VASHI----QSFLEVSYVRLHL 171
Dy	207	IKEITMHLRDLTSFNEKTVAVYL 233

RESULT 14
 ID 08MJ75 PRELIMINARY; PRT; 212 AA.
 AC 08MJ75;
 DT 01-OCT-2002 (TREMBrel. 22, Created)
 DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DR II-6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteraria; Cetartiodactyla; Sirenia; Suidae; Sub.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee D., Yoo H., Choi I.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF518322; BAM74938.1; -.
 DR HSSP: P02231; ILAU.
 GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; F:cytokine activity; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR009079; 4 helix cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF0049; IL6; 1.
 DR PRINTS: PR0043; IL6GCSFMG.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PRODOM: PD00435; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE 212 AA; 238.1 MW; 81CC85CCEB0389C4 CRC64;
 SQ

Query Match 12.3%; Score 110.5; DB 2; Length 212;
 Best Local Similarity 23.3%; Pred. No. 0.052;
 Matches 37; Conservative 32; Mismatches 85; Indels 5; Gaps 3;

Query Match 12.1%; Score 108; DB 2; Length 208;
 Best Local Similarity 21.3%; Pred. No. 0.086; Mismatches 81; Indels 6; Gaps 2;

Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

Query Match 21 VRKIQGDGAQLEKUCATYKUCHPERLVVGHSLGP-WAPLSSCPSPQLQLAGCLSQLH 79
 Best Local Similarity 21.1%; Pred. No. 0.086; Mismatches 81; Indels 6; Gaps 2;

Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

Query Match 80 SGFLFLQGLIQALEGISPELGPDTLQLDVAFTTIWQOMEELGMAPALQPT- 136
 Best Local Similarity 21.1%; Pred. No. 0.086; Mismatches 81; Indels 6; Gaps 2;

Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

Query Match 112 TGLLYQIVIYDLYQNEYEGDKGSIAEVQISIKAQILQKVKNPDEVTPDPTINASLM 171
 Best Local Similarity 21.1%; Pred. No. 0.086; Mismatches 81; Indels 6; Gaps 2;

Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

Query Match 137 -MPAFASAFORRAGGVVASHIQLQSLEYSYVR 169
 Best Local Similarity 21.1%; Pred. No. 0.086; Mismatches 81; Indels 6; Gaps 2;

Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

Query Match 172 NNLSQNDMMRNTKILLRSLENFLQSLRAIR 206
 Best Local Similarity 21.1%; Pred. No. 0.086; Mismatches 81; Indels 6; Gaps 2;

Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

Search completed: July 9, 2005, 12:53:58
 Job time : 112.181 secs

RESULT 15
 ID Q9XT80 PRELIMINARY; PRT; 208 AA.
 AC Q9XT80;
 DT 01-NOV-1999 (TREMBrel. 12, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)
 DE Interlein 6.
 OS Delphinapterus leucas (Beluga whale).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Monodontidae; Delphinapterus;
 OX NCBI_TaxID=9749;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20141864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6;
 RA St-Laurent G., Archambault D.;
 RT "Molecular cloning, phylogenetic analysis and expression of beluga
 whale (Delphinapterus leucas) interleukin 6.";
 RL Vet. Immunol. Immunopathol. 73:31-44(2000).
 DR EMBL: AF076643; ADD42929.1; -.
 DR HSSP; P05231; 1ALU.
 DR GO: GO:0005576; C:extracellular; IEA.

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OM protein - protein search, using SW model

Run on: July 9, 2005, 12:35:24 ; Search time 13.5387 Seconds

(without alignments)
1243.691 Million cell updates/sec

Title: US-10-750-797-2
 Perfect score: 901
 Sequence: MTPLGPASSLQSPFLKCLB.....SHLQSFLEVSYVRHLAQP 175

Scoring table: BLASTm62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 79;*

- 1: pir1;*
- 2: pir2;*
- 3: pir3;*
- 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query	Match Length	DB ID	Description
RESULT 1					
1	896	99.4	204	I_FRHUGL	POHUGL
2	884.5	98.2	207	2_A24573	granulocyte colony-stimulating factor precursor - human
3	744	82.6	194	2_TO9255	C;Species: Homo Sapiens (man)
4	738	81.9	174	2_TD0268	C;Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004
5	642	71.3	208	2_A26496	C;Accession: A25093; A49796; R47587; S68331
6	635	70.5	214	1_JC5043	R;Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.; BMB J. 5, 575-581, 1986
7	304	33.7	201	2_A42247	A;Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stimulating factor
8	106.5	11.8	212	2_I46590	A;Reference number: A25093; MUID:86220137; PMID:2423327
9	106.5	11.8	212	2_I46621	A;Accession: A25093
10	100	11.1	208	2_I09216	A;Molecule type: DNA; mRNA
11	94	10.4	345	2_C02270	A;Residues: 1-204 <NG>
12	89.5	9.9	2175	1_S03170	A;Cross-references: UNIPROT:P09919; EMBL:X03656; EMBL:X03655; NID:93169; PIDN:CAA27290
13	88.5	9.8	666	2_A87577	R;Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.
14	88.5	9.8	786	2_F83292	J. Leukoc. Biol. 41, 300-306, 1987
15	86	9.5	208	1_A56610	A;Title: Expression of granulocyte colony-stimulating factor by human cell lines.
16	86	9.5	502	2_S4652	A;Accession: A49796; MUID:87196936; PMID:3494801
17	85	9.4	207	2_I46084	A;Molecule type: mRNA
18	84	9.3	274	1_C69362	A;Residues: 1-204 <DEV>
19	83.5	9.3	846	2_JC7721	A;Cross-references: GB:M17706; NID:9183040; PIDN:AAA35882.1; PID:9183041
20	80.5	8.9	406	2_BT2766	R;Souza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Murdock, D.C.; Chazi
21	80	8.9	474	2_D75550	Science 232, 61-65, 1986
22	80	8.9	477	2_I46304	A;Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and
23	79.5	8.8	351	2_IT9623	A;Reference number: A47587; MUID:86151684; PMID:2420009
24	79	8.8	423	1_AC3553	A;Molecule type: mRNA
25	78	8.7	208	1_S29549	A;Accession: 19-204 <SOU>
26	78	8.7	316	2_H82958	A;Cross-references: GB:M13008; NID:9183044; PIDN:AAA03056.1; PID:9183045
27	77.5	8.6	653	2_C82580	R;Hanju, M.; Horan, T.; Arakawa, T.; Ie, J.; Katta, V.; Rohde, M.F.
28	77	8.5	974	2_AQ22076	Arch. Biochem. Biophys. 324, 344-356, 1995
29	76.5	8.5	195	2_JH0680	A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.

probable squalene hypothetical prote aryl hydrocarbon receptor probable threonyl-protein kinase probable D-Dalanyl-hypothetical prote hypothetical prote interleukin-11 precursor probable ATP-binding cassette RNA methyltransferase polyprotein - part interleukin-11 precursor hypothetical prote hypothetical prote interleukin-6 precursor probable oxidoreductase aryl hydrocarbon receptor cyclin-dependent kinase hypothetical prote virulence regulator

Query Match 99.4%; Score 896; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3_7e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 174; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 2 TPIGLPASSIPOSFILKLCIQRVKIQGDGAQLEKICATYKUCHREBLVILGHSGIPWAP 61
 Db 31 TPIGLPASSIPOSFILKLCIQRVKIQGDGAQLEKICATYKUCHREBLVILGHSGIPWAP 90
 C;Species: Homo sapiens (man)
 Qy 62 LSSCPSQALQAGLSQLHSGFLYQGLQALEGISPELGPTLTDQIADFATTWQ 121
 Db 91 LSSCPSQALQAGLSQLHSGFLYQGLQALEGISPELGPTLTDQIADFATTWQ 150
 Qy 122 MEELGMAPALQOPTOGAMPAFAASAFORRAGGVVLVASHLSFLEVSYVRHLAQ 175
 Db 151 MEELGMAPALQOPTOGAMPAFAASAFORRAGGVVLVASHLSFLEVSYVRHLAQ 204

RESULT 2

A24573 granulocyte colony-stimulating factor precursor variant splice form CHU-2 - human
 N;Alternate names: colony-stimulating factor 3; G-CSF
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C;Accession: A24573
 A;Title: Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor.
 R;Nagata, S.; Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Y.
 A;Reference number: A24573; MUID:86118679; PMID:3484805
 A;Accession: A24573
 A;Molecule type: mRNA
 A;Residues: 1-207 <NAG>
 A;Cross-references: UNIPROT:F09919; EMBL:X03438; PIDN:CAA2168.1; PID:g3190
 C;Comment: This variant splice form is not expressed in three other cell lines and may be a pseudogene.
 C;Genetics:
 A;Gene: GDB:CSF3
 A;Cross-references: GDB:112083; OMIM:138970
 A;Map position: 17q11.2-17q12
 A;Introns: 14/1; 68/3; 104/3; 153/3
 A;Superfamily: interleukin-6
 C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-70/Product: granulocyte colony-stimulating factor variant splice form CHU-2 #status predicted <SIG>
 F;69-75, 97-107/disulfide bonds: #status predicted

Query Match 98.2%; Score 884.5; DB 2; Length 207;
 Best Local Similarity 98.3%; Pred. No. 4.7e-77; Mismatches 0; Indels 3; Gaps 1;
 Matches 174; Conservative 0; MisMatches 0; Indels 3; Gaps 1;

Qy 2 TPIGLPASSIPOSFILKLCIQRVKIQGDGAQLEKICATYKUCHREBLVILGHSGIP 58
 Db 31 TPIGLPASSIPOSFILKLCIQRVKIQGDGAQLEKICATYKUCHREBLVILGHSGIP 90
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Accession: T10268
 R;O'Brien, P.M.; Seow, H.F.; Rothel, J.S.; Wood, P.R.
 DNA Seq. 4, 339-342, 1994
 A;Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDNA.
 A;Reference number: Z17009; MUID:95102116; PMID:7528579
 A;Accession: T10268
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residues: 1-174 <OBR>
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:Q28746; EMBL:1107939; NID:9310381; PIDN:AAA68006.1; PID:g3102
 C;Genetics:
 A;Gene: CSF
 C;Punction:
 A;Description: stimulates the differentiation and proliferation of hematopoietic progenitor cells
 C;Superfamily: interleukin-6
 C;Keywords: cytokine; growth factor; macrophage

Query Match 81.9%; Score 738; DB 2; Length 174;
 Best Local Similarity 82.2%; Pred. No. 3_7e-63; Mismatches 10; Indels 0; Gaps 0;
 Matches 143; Conservative 10; MisMatches 21; Indels 0; Gaps 0;

Qy 59 WAPLSSCPSQALQAGLSQLHSGFLYQGLQALEGISPELGPTLTDQIADFATTI 118
 Db 91 WAPLSSCPSQALQAGLSQLHSGFLYQGLQALEGISPELGPTLTDQIADFATTI 150
 Qy 119 WQMEELGMAPALQOPTOGAMPAFAASAFORRAGGVVLVASHLSFLEVSYVRHLAQ 175
 Db 151 WQMEELGMAPALQOPTOGAMPAFAASAFORRAGGVVLVASHLSFLEVSYVRHLAQ 207

RESULT 3

T09255 granulocyte colony-stimulating factor precursor - cat (fragment)
 C;Species: Felis silvestris catus (domestic cat)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09255
 R;Dunham, S.P.; Onions, D.E.
 A;Description: Cloning, sequence and expression of feline granulocyte colony stimulating factor.
 A;Reference number: Z16630
 A;Accession: T09255
 A;Status: preliminary; translated from GB/EMBL/DDBJ

RESULT 4

T10268 granulocyte colony-stimulating factor - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Accession: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 R;Seow, H.F.; Rothel, J.S.; Wood, P.R.
 DNA Seq. 4, 339-342, 1994
 A;Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDNA.
 A;Reference number: Z17009; MUID:95102116; PMID:7528579
 A;Accession: T10268
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residues: 1-174 <OBR>
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:Q28746; EMBL:1107939; NID:9310381; PIDN:AAA68006.1; PID:g3102
 C;Genetics:
 A;Gene: CSF
 C;Punction:
 A;Description: stimulates the differentiation and proliferation of hematopoietic progenitor cells
 C;Superfamily: interleukin-6
 C;Keywords: cytokine; growth factor; macrophage

Query Match 81.9%; Score 738; DB 2; Length 174;
 Best Local Similarity 82.2%; Pred. No. 3_7e-63; Mismatches 10; Indels 0; Gaps 0;
 Matches 143; Conservative 10; MisMatches 21; Indels 0; Gaps 0;

Qy 2 TPIGLPASSIPOSFILKLCIQRVKIQGDGAQLEKICATYKUCHREBLVILGHSGIPWAP 61
 Db 1 TPIGLPASSIPOSFILKLCIQRVKIQGDGAQLEKICATYKUCHREBLVILGHSGIPWAP 60
 Qy 62 LSSCPSQALQAGLSQLHSGFLYQGLQALEGISPELGPTLTDQIADFATTWQ 121
 Db 61 LSSCPSQALQAGLSQLHSGFLYQGLQALEGISPELGPTLTDQIADFATTWQ 120

Qy 122 MEELGMAPALQOPTOGAMPAFAASAFORRAGGVVLVASHLSFLEVSYVRHLAQ 175
 Db 121 MEDLGAVAPQPTGTMFTSAFORRAGGVVLVASHLSFLEVSYVRHLAQ 174

RESULT 5

A26496 granulocyte colony-stimulating factor precursor - mouse
 N;Alternate names: G-CSF
 C;Species: Mus musculus (house mouse)
 C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
 C;Accession: A29536; A26496; S02493

C;Genetics: IL-6
A;Gene: IL-6
C;Superfamily: interleukin-6

Query Match 11.8%; Score 106.5; DB 2; Length 212;
Best Local Similarity 22.6%; Pred. No. 0.0094; Mismatches 85; Indels 5; Gaps 3;
Matches 36; Conservative 33; Mismatches 85; Indels 5; Gaps 3;

Qy 17 KOLEQRKIQLOGALQELKCATYKLCPPEVLGHSLGIP-WAPLSSCPSQLQAGC 75
Db 52 KTEELIKVILGKISAMRKEMCKEKECENSKEVLAENNLNLPKAEDKGCFOSGFNGETC 111

Qy 76 ISQLHSGIPLFLQGILQALEGISPLGLPTLTDLOLDVADFAATTWQOMEELGMAPALOPT- 134
Db 112 LMRITGIVVERQIYLQKEYESNKGNVTEAVISTKALIQTLRQGSKNPDKATTNPPT 171

Qy 135 -QGAMPAPAS-AFORRAGGVLYASHIQLQSLEVSYVR 170
Db 172 NAGLDDKLUQSONEWMMNTKILILIRSLDFQFSLRAIR 210.

RESULT 9

I46621L
prointerleukin 6 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: I46621

R;Richards, C.; Saklatava, J.

Cytokine 3, 269-276, 1991

A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of Reference number: I46621; MUID:9138547; PMID:1873476

A;Accession: I46621

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-212 <RC>

A;Cross-references: UNIPROT:P26893; GB:MB6722; NID:9164624; PIDN:AC37333.1; PID:9164625

C;Genetics: IL-6

C;Superfamily: interleukin-6

C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor

Query Match 11.1%; Score 10; DB 2; Length 208;
Best Local Similarity 21.6%; Pred. No. 0.038; Mismatches 95; Indels 8; Gaps 3;
Matches 38; Conservative 35; Mismatches 95; Indels 8; Gaps 3;

Qy 3 PIGPASSLPPSPL---KCUBQRKIQGDGAQELKCATYKLCPPEVLGHSLGIP 58
Db 31 PIGDEDETSNPSPLTADTKTKHIIKYLGKISALKHNMNNFSKCNSKEYLAENNLLP 90

Qy 59 -WAPLSSCPSQLQAGCLSQLQHSGIPLFLQYQIQLQALEGISPLGLPTLTDLOLDVADFAATT 117
Db 91 KNAEKDGGCPQSGFNQETCLMKITTGISEFQYLEVQNEPKGEKENIKTKISTKLVQI 150

Qy 118 IWQOMEELGMA--PALOPTQGAMPAPASAFORRAGGVLYASHIQLQSLEVSYVR 170
Db 151 INQKMKNPVEVTTPDTAKSSILAKHSQNEMLKNTTTHLRSLENPLQFSLRAIR 206

RESULT 11

C82270

hypothetical protein VC0086 [imported] - vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: C82270

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chadron, D.; Ermoljeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: C82270

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <RC>

A;Cross-references: UNIPROT:Q0KTL6; GB:AE004172; GB:AE003852; NID:99655323; PIDN:AAF9404

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

A;Genetics: VC0086

A;Map position: 1

Query Match 10.4%; Score 94; DB 2; Length 345;

Best Local Similarity 32.2%; Pred. No. 0.26; Mismatches 43; Indels 22; Gaps 6;

Matches 38; Conservative 15; Mismatches 43; Indels 22; Gaps 6;

Qy 8 SSLPOSPLKLCLEQRKIQLOGALQELKLC--ATYKLCPPEVLGHSLGIPWAPS 63
Db 228 ASDPDPLFLAAL--VKAAGAPANTIDATCDAILASPACHPEVIALA--GRSMWLSLE 282

Qy 64 S--CPSQALQAGLCSQ-LHSGFLXQGLQIALEGI-----SPELGPTLQ 108
Db 283 NSGRAQRPLIRIAQTONQPIENOLFADVVMLPALRGVMPILHASPSPELAQECQ 340

Db 172 NAGLDDKLUQSONEWMMNTKILILIRSLDFQFSLRAIR 210

RESULT 12

S03170

homeotic protein cut - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Accession: S03170

R;Blochlinger, K.; Bodmer, R.; Jack, J.; Jan, L.Y.; Jan, Y.N.

Nature 333, 628-635, 1988

A;Title: Primary structure and expression of a product from cut, a locus involved in ape submitted to the EMBL Data Library, July 1996

A;Reference number: S03170; MUID:88232956; PMID:2897632

A;Accession: S03170

A;Molecule type: mRNA

A;Residues: 1-217 <RC>

A;Cross-references: UNIPROT:P10180; EMBL:X07985; NID:97767; PIDN:CAA30794.1; PID:97768

A;Gene: cut

A;Cross-references: Flybase:FBgn0004198

A;Superfamily: homeotic protein cut; cut repeat homology; homeobox homology

A;Gene: IL-6

C;Genetics:

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: F83292
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin, J.; Lory, S.; Olsen, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A02950; MUID:20437337; PMID:10984043
 A;Accession: F83292
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-786 <STO>

Query Match 9.9%; Score 89.5; DB 1; Length 2175;
 Best Local Similarity 23.8%; Pred. No. 6.7; Matches 35; Conservative 20; Mismatches 61; Indels 31; Gaps 3; Query 28 DGAALQEKUCHTYKUCHPPEELVILGLHSIGLWQMP-----0 1404 DENAVTHKLVASHQYKIA-PEKLMRTGSYSQSPOMP-----0 1437
 QY 88 GLLQALEGGSPELGPTLDTIQLQDVAFTTIQWQMEBELGMAPALOPTQAMPAFASAFQR 147
 Db 1438 GLASKRQMAASIPMQRMSELQEQPRAQAHQJMQMQMORAAAMSAMQQQ----VAQAQQ 1492
 QY 148 RAGSVLVASHQOSFLEVSYRFLRHQ 174
 Db 1493 AQQAQQAQHQHLLQQAQAOHQHLLQQHQH 1519

RESULT 13

A87577 oligopeptide transporter, OPR family CC2646 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus
 C;Accession: A87577
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon, N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Status: preliminary

A;Accession: A87577

A;Molecule type: DNA

A;Residues: 1-666 <STO>

A;Cross-references: UNIPROT:Q9A523; GB:AE005673; NID:913424225; PIDN:AAK24613.1; GSPDB:Q

C;Genetics:

A;Gene: CC2646

C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0361

Query Match 9.8%; Score 88.5; DB 2; Length 666;

Best Local Similarity 32.5%; Pred. No. 2; Matches 37; Conservative 14; Mismatches 48; Indels 15; Gaps 4;

Db 51 LGHSQGIPWAPLSSCPSSQALQAGLUSQLSLFLYQGQQLQALSGCISPELGPTLDTIQLQDVAFTTIQWQMEBELGMAPALOPTQAMPAFASAFQR 110
 196 LGAAAGATGIGASS--SLAAGMAGHLMGTVGVAMFTGIFTAWAIIVLPIITLVTLPMPED 253

QY 111 VADPATTWQ-QMELG-----MAPPALQP-TQGAMPAFASAFQRAGG 151
 Db 254 AATHALTWWSQVRPLLAGVIGAAAIWTLAKLVGPITSGLKSAFAAQARKAGG 307

RESULT 14

F83292 probable sensor/response regulator hybrid PA2824 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C;Species: *Pseudomonas aeruginosa*
 C;Accession: F83292

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin, J.; Lory, S.; Olsen, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen

A;Reference number: A02950; MUID:20437337; PMID:10984043

A;Accession: F83292

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-786 <STO>

A;Cross-references: UNIPROT:P26832; EMBL:X37317; NID:92193; PIDN:CAA40572.1; PID:92194
 A;Experimental source: BLV induced B cell lymphosarcoma
 A;Note: Sequence extracted from NCBI backbone (NCBIP:118917)
 C;Keywords: cytokine

Query Match 9.5%; Score 86; DB 1; Length 208;
 Best Local Similarity 20.5%; Pred. No. 0.83; Matches 36; Conservative 37; Mismatches 95; Indels 8; Gaps 3; Query 3 PLG---PASSLPOSFLIKLEQ---VRKIQDGQALBKLCATYKUCHPPEELVILGHSL 55
 Db 31 PLGSDPKDNTTPPERLITTPKEKTVBALIKRWDKISAMKEICKEKNDEGESKETLAENKL 90
 QY 56 GIP-WAPLSSCPSSQALQAGLUSQLSLFLYQGQQLQALSGCISPELGPTLDTIQLQDVAFTTIQWQMEBELGMAPALOPTQAMPAFASAFQRAGG 114
 Db 91 NLPRMEBEDGCFQSGFNQDCLIRTTAGLEYQYIYDLYQNEYEGQNENVRDIRKNTL 150
 QY 115 ATTWQMEBELGMAPALOPTQAMPAFASAFQRAGGTVLASHQOSFLEVSYVLR 170
 Db 151 IOILQKQAKDLITTPATNDLLEKMQSSNEWVNKAQKILILRNLENFLQPSLRAIR 206

Search completed: July 9, 2005, 12:45:23
 Job time : 14.5387 sec

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Date: July 9, 2005, 12:41:15 ; Search time 111.819 Seconds
(without alignments)
801.415 Million cell updates/sec

Query: US-10-750-797-2
Sequence: I MTPIGPASLIPQSFILKLCR.....SHLASFLEVLSVIRVHLAQ P 175

Title: perfect score:
Score: 901

Searcher: BLOSUM62
Gapop: 10.0 , Gapext: 0.5

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Query	Length	DB	ID	Description
1	896	99.4	200	2	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.2	207	1	CSF3_HUMAN	Q8N4W3 homolog (99%), human
3	744	82.5	194	1	CSF3_FELCA	Q8N4W3 felis silvestris catus
4	744	82.6	195	2	Q9GUU0	Q8N4W3 felis silvestris catus
5	739	82.0	175	1	CSF3_CANFA	Q8N4W3 canis familiaris
6	738	81.9	174	1	CSF3_SHEEP	Q8N4W3 ovis aries
7	727	80.7	195	1	CSF3_BOVIN	Q8N4W3 bovis taurinus
8	702	77.9	195	1	CSF3_PIG	Q8N4W3 sus scrofa
9	692	71.3	208	1	CSF3_MOUSE	Q8N4W3 mus musculus
10	635	70.5	214	2	P97712	Q8N4W3 rattus norvegicus
11	511	56.7	127	2	Q8MK60	Q8N4W3 equus caballus
12	304	33.7	201	1	MGP_CHICK	Q8N4W3 gallus gallus
13	111	12.3	241	2	Q90710	Q8N4W3 gallus gallus
14	110.5	12.3	212	2	Q8WU75	Q8N4W3 sus scrofa
15	108	12.0	208	2	Q9XT80	Q8N4W3 delphinapterus leucas
16	106.5	11.8	212	1	IL6_PIG	Q8N4W3 sus scrofa
17	101	11.2	205	1	IL6_ORCOR	Q8N4W3 orcinus orca
18	100	11.1	208	1	IL6_HORSE	Q8N4W3 equus caballus
19	96	10.7	189	2	Q6M282	Q8N4W3 homo sapien
20	96	10.7	189	2	Q8H2A5	Q8N4W3 homo sapien
21	95	10.5	208	1	IL6_FELCA	Q8N4W3 felis silvestris catus
22	94.5	10.5	455	2	Q8DT06	Q8N4W3 vulpes vulpes
23	94	10.4	345	2	Q8KTM6	Q8N4W3 vibrio cholerae
24	93	10.3	189	2	Q9NEP7	Q8N4W3 homo sapien
25	91	10.1	189	2	Q6N280	Q8N4W3 homo sapien
26	89.5	9.9	214	2	Q8H2E5	Q8N4W3 sus scrofa
27	89.5	9.9	215	1	HMCU_DROME	Q8N4W3 drosophila melanogaster
28	88.5	9.8	666	2	Q9A523	Q8N4W3 caulosphaera sp.
29	88.5	9.8	786	2	Q9T019	Q8N4W3 pseudomonas aeruginosa
30	88.5	9.8	1931	2	Q8RJY3	Q8N4W3 stigmatostigmaria
31	88	9.8	290	2	Q9BPS7	Q8N4W3 apicomplexa

SEARCHED: 1612378 seqs, 51.2079187 residues

RESULTS: 1612378

SEARCH TIME: 111.819 Seconds

SEARCHER: BLOSUM62

ALIGNMENTS: 175

OPTIM: Q8tth4 actobius nigri

DR PRINTS; PR00434; INTERLEUKIN6.
 DR PRODOM; PDD08388; GCSF MGF; 1.
 DR PRODOM; PDD04356; Interleukin_6; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PR00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 200 AA; 21543 MW; 864A855B329A96C CRC64;
 Query Match 99.4%; Score 896; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 6 9e-74;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 TRIGPASLIPQESTLKLQEQVKRKGALQKLCATYKLCIPEELVLAGHSLGTLWAP 61
 Db 27 TPLGPASSLIPQESTLKLQEQVKRKGALQKLCATYKLCIPEELVLAGHSLGTLWAP 86
 Qy 62 LSCPSQLQLACLSQHSGLYQGLQALSGISPLGPTDQLDVAARATWQ 121
 Db 87 LSCPSQLQLACLSQHSGLYQGLQALSGISPLGPTDQLDVAATWQ 146
 Qy 122 MEBLGMAPALQPTQGAMPAFAAFORRAGGVLYASHIQSFLVEYSYRVRHLAQ 175
 Db 147 MEBLGMAPALQPTQGAMPAFAAFORRAGGVLYASHIQSFLVEYSYRVRHLAQ 200
 RESULT 2
 CSF3 - HUMAN STANDARD; PRT; 207 AA.
 AC P09919;
 ID 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoietin)
 DE (Filgrastim) (Lenograstim).
 GN Name=CSF3;
 OS Homo sapiens (Human).
 OC Buka-Ytota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=86118679; PubMed=3484805;
 RX MEDLINE=86118679; PubMed=7518249;
 RA Nagata S., Kubota N., Oheda M., Nomura H., Kaziro Y., Yamamoto O.,
 RA Hirata Y., Kubota N., Oheda M., Nomura H., Yamamoto O., Hirata Y.,
 RT "Molecular cloning and expression of cDNA for human granulocyte
 RT colony-stimulating factor";
 RL Nature 319:415-418 (1986).
 RN [2]
 SEQUENCE FROM N.A.
 RP RX MEDLINE=86220137; PubMed=2423337;
 RA Nagata S., Tsuchiya M., Kano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamamoto T.;
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 RT colony-stimulating factor.";
 RL EMBO J. 5:55-81(1986).
 RN [3]
 SEQUENCE FROM N.A.
 RP RX MEDLINE=87196936; PubMed=3494801;
 RA Devlin J.-J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 RT lines";
 RL J. Leukoc. Biol. 41:302-306(1987).
 RN [4]
 SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs. NHBLI HU66692 program for genomic applications, UW-
 RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>);
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE=86151684; PubMed=2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,

RJ Murdoch D.C., Chaazin V.R., Bruszewski J., Lu H., Chen K.K.,
 RA Barrientos J., Platzer B., Moore M.A.S., Mertelmann R., Welte K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.",
 Science 232:61-66(1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=93293947; PubMed=7685769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 produced in Chinese hamster ovary cells";
 RL J. Chromatogr. A 637:55-62(1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-M;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 derived from NMR spectroscopy";
 RL FEBS Lett. 314:435-439 (1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94304855; PubMed=7518249;
 RA Zink T., Ross A., Lueras K., Cieslar C., Rudolph R., Holak T.A.;
 RT "structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 bundle protein";
 RL Biochemistry 33:8453-8463 (1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93281718; PubMed=7685117;
 RA Hill C.P., Osslund T.D., Bisemburg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 relationship to other growth factors";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
 CC -I- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSR induces granulocytes.
 CC -I- SUBUNIT: Monomer.
 CC -I- ALTERNATIVE LOCATION: Secreted.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoID=P09919-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoID=P09919-2; Sequence=VSP_002673;
 CC -I- PRM: O-glycan consists of Gal-GalNAc disaccharide which can be
 CC modified with up to two sialic acid residues (done in
 CC recombinantly expressed G-CSF from CHO cells).
 CC -I- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -I- CAUTION: Ref.4 misquotes the gene name as "CSF1".
 CC -I- DATABASE: NAME=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW="<http://www.neupogen.com/>".
 CC -----
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 CC -----
 DR EMBL; X03438; CAA27168.1; --.
 DR EMBL; M13008; AAA03056.1; --.
 DR EMBL; X03556; CRA27291.1; --.
 EMBL; X03655; CAA27290.1; --.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95102116; PubMed=7528579;
 RA O'Brien P.M.; Seow H.F.; Rothel J.S.; Wood P.R.;
 RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
 factor cDNA." DNA seq. 4:339-342(1994).
 CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes (BY similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-Glycosylated (BY similarity).
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMAIL: 107939; AAA88006.1; -.
 DR PIR: TI0261; TI268.
 DR HSPB; P09919; IHRG.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSF MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR PRINTS; PR0433; IL6GSFMGF.
 DR PRODOM; PDD08388; GCSF MGF; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor.
 FT DISULFD 36 42 BY similarity.
 FT DISULFD 64 74 BY similarity.
 FT CARBOHD 133 133 O-linked (GALNAc. . .) (BY similarity).
 FT SEQUENCE 174 AA; 18806 MW; BASA8P8D23ACDIE CRC64;
 Query Match Best Local Similarity 81.9%; Score 738; DB 1; Length 174;
 Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;
 Qy 2 TRIGPASSLQPSFLKLCLEQRVKIQGDGAQLEKCATYKLCRPERLVLGHSLGIPAP 61
 Db 1 TPLGPARSILPOSFLKLCLEQRVKIQDAGABEQLERLCAHKLCHPEBLVIGHSLGIPAP 60
 Qy 62 LSSCPSQLQLAGLSQLHSGLFLYQGLQALEGISPELGPDTLQDVAFTTIWQ 121
 Db 61 LASCCSDPSLQTSCLDQHQGLFLYQGLQALEGISPELAPTDTLQDVTATNIWQ 120
 Qy 122 MEDLGMAPALQOPTOGAMPAFASAORRAGGVVASHQSFLYESYRVRLHQ 175
 Db 121 MEDLGAVAPAVQPIQGTMPTFTAQFRRAGGVVLAQLOFLGLAYRGRLYLP 174
 RESULT 7
 CSP3_BOVIN ID CSP3_BOVIN STANDARD; PRT; 195 AA.
 AC P35833; OPTV89;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 DE Name=CSF3; Synonyms=CSF;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteraria; Getaiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxId=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95102116; PubMed=7528579;
 RA Heidari M.; Kehrli M.E. Jr.;
 RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
 colony stimulating factor." Submitted (SBB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=94076341; PubMed=7504736;
 RA Lovejoy B.; Cascio D.; Eisenberg D.;
 RT "Crystal structure of canine and bovine granulocyte-colony stimulating
 factor (G-CSF)." J. Mol. Biol. 234:640-653 (1993).
 CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-Glycosylated.
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMAIL: AF09233; AAD1602.1; -.
 DR PDB; 18SC; X-ray; @=22-195.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR PRODOM; PDD08388; GCSF MGF; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR PRINTS; PR0433; IL6GSFMGF.
 DR PRODOM; PDD08388; GCSF MGF; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 195 Granulocyte colony-stimulating factor.
 FT DISULFD 57 63
 FT DISULFD 85 95 O-linked (GALNAc. . .) (BY similarity).
 FT CARBOHD 154 154 TS -> RG (in Ref. 2).
 FT CONFLICT 93 94
 FT HELIX 32 60
 FT HELIX 65 69
 FT TURN 70 71
 FT HELIX 72 75
 FT TURN 76 76
 FT HELIX 83 85
 FT TURN 87 89
 FT HELIX 92 112
 FT TURN 113 115
 FT TURN 118 120
 FT HELIX 121 121
 FT HELIX 164 191
 FT TURN 192 192
 SQ SEQUENCE 195 AA; 21431 MW; BC06119E4ADFBAT3 CRC64;
 Query Match Best Local Similarity 80.7%; Score 727; DB 1; Length 195;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 Qy 2 TPLGPASSLQPSFLKLCLEQRVKIQDAGABEQLERLCAHKLCHPEBLVIGHSLGIPAP 61
 Db 22 TPLGPARSILPOSFLKLCLEQRVKIQDAGABEQLERLCAHKLCHPEBLVIGHSLGIPAP 81

DR InterPro: IPR003629; GCSF MGF.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR PFam: PF00489; IL6; 1.
 DR PRINTS: PR00433; ILGCSFMGF.
 DR Prodrom; PDD008388; GCSF MGF; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Direct protein sequencing; Glycoprotein; Growth factor;
 KW Signal.
 FT CHAIN 31 30 Granulocyte colony-stimulating factor.
 FT DISUFD 72 78 By similarity.
 FT DISUFD 100 110 By similarity.
 FT CARBHYD 169 169 O-linked (GalNAc...) (By similarity).
 SQ SEQUENCE 208 AA; 22421 MW; 0B3622135C906DB CRC64;

Query Match Best Local Similarity 74.6%; Pred. No. 1. 2e-50; Length 208; Matches 129; Conservative 11; Mismatches 33; Indels 0; Gaps 0; OQ 1 MTPIGPASSLQSPFLKLCLEVKRKGCGDGAQELQEKUCATYKUCHPEERLVGHSGLIPWA 60
 36 VSALPPSLPLRSFLRKTSQPLKQGKQGKQGLQGKQGLQGKQGLQGKQGLQGKQGLQGKQ 95
 61 PLSSCPSQLQLAGCLSQLHSGLFLYQGLQALEGSISPELGPFTLQDVAFTIWIQ 120
 96 SLSGGESSOQALQOTCISQLSHGGLCQGLQGLQGLQGLQGLQGLQGLQGLQGLQGLQ 155

Db 121 QMERLGMAPAQOPTQAMPAPASAFAORRAGGVLYVASHLQSTLEVSVIRHLAOP 175
 156 QMENLIGVAPTQOPTOSAMPATSAFORRAGGVLYVASHLQSTLEVSVIRHLAOP 208

RESULT 10
 P97112 PRELIMINARY; PRT: 214 AA.
 AC P97112;
 DT 01-MAY-1997 (TREMBrel. 03, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Granulocyte colony stimulating factor.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Noromita L.E.; Takakuji V.A., Sharova I.V., Cristman M.V., Howard R.D.;
 RR Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF00365; AMM34205.1; .
 DR HSSP; P3833; IBGC.
 GO; GO:0005576; C:extracellular.
 DR GO; GO:0005125; P:cytokine activity; IEA.
 DR GO; GO:0008083; P:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSF MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR PFam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR Prodrom; PDD008388; GCSF MGF; 1.
 DR SMART; SNO0116; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE; 214 AA; 23659 MW; 29B888B17B684C55 CRC64;

Query Match Best Local Similarity 79.5%; Pred. No. 7e-39; Length 127; Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0; OQ 49 VLHSGLIGPAPWSSCPSQLQLAGCLSQLHSGLFLYQGLQALEGSISPELGPFTLQDVAFTIWIQ 108
 1 MILGKSLGIGIPOPLISLSSCQALQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQ 60
 Db 109 LDVADFATTIWIQMEBLGMAPAQOPTQAMPAPASAFAORRAGGVLYVASHLQSTLEVSVIRHLAOP 168
 61 LDVADFATTIWIQMEBLGMAPAQOPTQAMPAPASAFAORRAGGVLYVASHLQSTLEVSVIRHLAOP 108
 OQ 169 LRHLAQP 175
 Db 121 LRHLAQP 127

RESULT 12
 MGF_CHICK ID MGF CHICK STANDARD; PRT: 201 AA.
 AC P13854;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Myelomonocytic growth factor precursor (MGF).
 OS Gallus gallus (Chicken).

Query Match 70.5%; Score 635; DB 2; Length 214; Best Local Similarity 72.6%; Pred. No. 5.6e-50; Mismatches 36; Indels 0; Gaps 0;

Matches 127; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

Q8MUT5; PRELIMINARY; PRT; 212 AA.
 ID Q8MUT5; PRELIMINARY; PRT; 212 AA.
 AC Q8MUT5; PRELIMINARY; PRT; 212 AA.
 DT 01-OCT-2002 (TREMBREL; 22, Last sequence update)
 DT 01-MAR-2004 (TREMBREL; 26, Last annotation update)
 DR IL-6.
 OS Sub scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Buteraria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TAXID=9823;
 [1] SEQUENCE FROM N.A.
 RP Lee D.; Yoo H.; Choi I.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AFB1832; AAM74938.1; -.
 DR HSSP; P05231; iALU.
 GO; GO:0005575; C:extracellular; IEA.
 GO; GO:0005125; F:cytokine activity; IEA.
 GO; GO:0005138; F:cytokine receptor binding; IEA.
 GO; GO:0006955; Immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR03574; Interleukin_6.
 DR InterPro; IPR03574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFNGF.
 DR PRINTS; PR00424; INTERLEUKIN6.
 DR PRODOM; PDD004556; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 212 AA; 23881 MW; 1F540B7030BCFD77 CRC64;
 Query Match 12.3%; Score 108; DB 2; Length Best Local Similarity 21.3%; Pred. No. 0.088;
 Matches 37; Conservative 32; Mismatches 33; Indels 3; Gaps 3; :
 Db 52 KTEBLILKYLIGKISAMREEMCEKYKCKENSKEVLAENNLNPKQAEKDCFCQSGFNQETC 111
 Qy 17 KCLEQVKRCODGAALQOKLCATYKQCHPEELVULGLHSIGTP-WAPLSSCPSONAQLAGC 75
 Qy 76 LSQHISGLFLYQGLIQALEGISPELAGPTLDTIQLDADFTTIWQHEELGMAPPQPT- 134
 Db 112 LMRITTGVLBFQIYDLYQKEYESNKGNEVAOISTKRLQIQTIRQKGKNDPKRATTNPNTT 171
 Qy 135 -QGAMPAFAS--AFFRRAGGIVLVASHLQSFLVEVSYRVL 170
 Db 172 NAGILDKLQSONEWMKNTKILLRSLEDFLOFSLRAIR 210
 RESULT 15
 09XT80 PRELIMINARY; PRT; 208 AA.
 ID 09XT80; PRELIMINARY; PRT; 208 AA.
 AC 09XT80; PRELIMINARY; PRT; 208 AA.
 DT 01-NOV-1999 (TREMBREL; 12, Last sequence update)
 DT 01-MAR-2004 (TREMBREL; 26, Last annotation update)
 DE Interleukin 6.
 OS Delphinapterus leucas (Beluga whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Buteraria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monodontidae; Delphinapterus.
 OC NCBI_TAXID=9749;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-2011864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6;
 RA St-Laurent G.; Archambault D.;
 RT "Molecular cloning, phylogenetic analysis and expression of beluga
 whale (Delphinapterus leucas) interleukin 6.";
 RL Vet. Immunol. Immunopathol. 73:31-44(2000).
 EMBL; AP07643; AAB42929.1; -.
 DR HSSP; P05231; iALU.
 GO; GO:0005576; C:extracellular; IEA.